IN THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1 - 5 (canceled).

6 (currently amended). A method for identifying a protein that is differentially displayed in the mass spectra of two complex biologic samples, comprising:

(a) in parallel, adsorbing a subset of proteins from each of two complex biologic samples to an adsorptive surface of an affinity capture probe;

~~(a)~~ **(b)** ~~**with a mass spectrometer,**~~ detecting at least one protein that is differentially displayed in the **laser desorption ionization (LDI)** mass spectra of the two ~~**samples**~~ **adsorbed subsets**;

~~(b)~~ **(c)** cleaving proteins ~~**in the two samples**~~ **adsorbed to said probes** into protein cleavage products and ~~**with a mass spectrometer**~~ detecting protein cleavage products that are differentially displayed in the **LDI** mass spectra of the two cleaved ~~**samples**~~ **adsorbed subsets**;

~~(c)~~ **(d)** determining ~~**the**~~ **at least one** identity **candidate** ~~**of**~~ **for** at least one differentially displayed protein cleavage product with a tandem mass spectrometer; and

~~(d)~~ **(e)** correlating the **at least one** identity **candidate** ~~**of**~~ **for** the **at least one differentially displayed**

protein cleavage product **of step (d)** with a differentially displayed protein of step ~~(a)~~ **(b)**,

whereby the correlation identifies a ~~differentially displayed~~ protein **as had been differentially present in the two complex biologic samples**.

7 (currently amended). The method of claim 6 wherein:

~~(a)~~ **(b)** detecting comprises:

~~(i) capturing proteins from the samples on affinity capture probes;~~

~~(ii)~~ **(i)** analyzing the ~~captured~~ **adsorbed** proteins from each sample by laser desorption/ionization mass spectrometry;

~~(iii)~~ **(ii)** comparing the mass spectra of the ~~captured~~ **adsorbed** proteins in the two samples to identify proteins that are differentially displayed;

~~(b)~~ **(c)** cleaving and detecting comprises:

~~(i) capturing proteins from the samples on affinity capture probes;~~

~~(ii)~~ **(i)** generating protein cleavage products on the affinity capture probes using a proteolytic agent;

~~(iii)~~ **(ii)** analyzing the protein cleavage products by laser desorption/ionization mass spectrometry;

~~(iv)~~ **(iii)** comparing the mass spectra of the protein cleavage products in the two ~~samples~~ **adsorbed subsets** to

identify protein cleavage products that are differentially displayed; and

~~(c)~~ **(d)** determining **at least one** ~~the~~ identity **candidate** ~~of~~ for at least one differentially displayed protein cleavage product comprises:

(i) desorbing the protein cleavage products from the affinity capture probes into gas phase to generate corresponding parent peptide ions,

(ii) with a first mass spectrometer, selecting a differentially displayed parent peptide ion for subsequent fragmentation,

(iii) fragmenting the selected parent peptide ion under selected fragmentation conditions in the gas phase to produce product ion fragments with a second mass spectrometer,

(iv) generating a mass spectrum of the product ion fragments; and

(v) identifying at least one protein identity candidate for said differentially displayed cleavage product by submitting at least one product ion mass spectrum to a protein database mining protocol which identifies at least one protein identity candidate for the differentially displayed protein cleavage product based on a measure of closeness-of-fit between the product ion mass spectrum and theoretical mass spectra of proteins in the database.

8 (canceled).

9 (original). The method of claim 6 or 7 wherein the differentially displayed protein is detectable uniquely in one of said two samples.

10 (currently amended). The method of claim 6 or 7 wherein ~~(b)~~ **(c)** cleaving comprises enzymatic fragmentation.

11 (original). The method of claim 10 comprising limited enzymatic digestion.

12 (currently amended). The method of claim 6 or 7 wherein ~~(b)~~ **(c)** cleaving comprises chemical cleavage.

13 (previously presented). The method of claim 12 wherein chemical cleavage comprises acid hydrolysis.

14 (original). The method of claim 6 or 7 wherein the two samples are selected from (1) a sample from a healthy source and a sample from a diseased source, (2) a sample from a test model exposed to a toxic compound and a sample from a test model not exposed to the toxic compound or (3) a sample from a subject that responds to a drug and a sample from a subject that does not respond to the drug.

Claims 15 - 26 (canceled).